giime demux emp-paired \ --m-barcodes-file AliyaMetaDataNew.tsv \ --m-barcodes-column BarcodeSequence \ --p-rev-comp-barcodes \ --p-rev-comp-mapping-barcodes \ --i-seqs emp-paired-end-sequences.qza \ --o-per-sample-sequences demux-full-new.gza \ --o-error-correction-details demux-details-new.qza qiime demux summarize \ --i-data demux-full-new.gza \ --o-visualization demux-full-new.qzv ##### qiime dada2 denoise-paired \ --i-demultiplexed-segs demux-full-new.gza \ --p-trim-left-f 0 \ --p-trim-left-r 0 \ --p-trunc-len-f 195 \ --p-trunc-len-r 205 \ --o-table table.qza \ --o-representative-sequences rep-seqs.gza \ --o-denoising-stats denoising-stats.qza qiime feature-table summarize \ --i-table table.qza \ --o-visualization table.gzv \ --m-sample-metadata-file AliyaMetaDataNew.tsv qiime feature-table tabulate-seqs \ --i-data rep-seqs.qza \ --o-visualization rep-seqs.qzv qiime metadata tabulate \ --m-input-file denoising-stats.qza \ --o-visualization denoising-stats.qzv ######### qiime phylogeny align-to-tree-mafft-fasttree \ --i-sequences rep-seqs.qza \

--o-alignment aligned-rep-seqs.qza \

```
--o-masked-alignment masked-aligned-rep-segs.gza \
 --o-tree unrooted-tree.qza \
 --o-rooted-tree rooted-tree.gza
qiime diversity core-metrics-phylogenetic \
 --i-phylogeny rooted-tree.qza \
 --i-table table.gza \
 --p-sampling-depth 15500 \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --output-dir core-metrics-results
qiime diversity alpha-correlation \
 --i-alpha-diversity core-metrics-results/faith_pd_vector.gza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --o-visualization core-metrics-results/faith-pd-alpha-correlation.gzv
qiime diversity alpha-correlation \
 --i-alpha-diversity core-metrics-results/shannon vector.qza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --o-visualization core-metrics-results/shannon-group-correlation.gzv
qiime diversity alpha-group-significance \
 --i-alpha-diversity core-metrics-results/faith_pd_vector.gza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --o-visualization core-metrics-results/faith-pd-group-significance.qzv
qiime diversity alpha-group-significance \
 --i-alpha-diversity core-metrics-results/evenness vector.qza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --o-visualization core-metrics-results/evenness-group-significance.qzv
giime diversity beta-group-significance \
 --i-distance-matrix core-metrics-results/unweighted_unifrac_distance_matrix.qza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --m-metadata-column Stagnation \
 --o-visualization core-metrics-results/unweighted-unifrac-stagnation-group-significance.qzv \
 --p-pairwise
qiime diversity beta-group-significance \
 --i-distance-matrix core-metrics-results/unweighted_unifrac_distance_matrix.qza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --m-metadata-column Material \
 --o-visualization core-metrics-results/unweighted-unifrac-material-group-significance.qzv \
 --p-pairwise
```

```
giime diversity beta-group-significance \
 --i-distance-matrix core-metrics-results/unweighted_unifrac_distance_matrix.qza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --m-metadata-column Stagnation \
 --p-method 'permdisp' \
 --o-visualization core-metrics-results/unweighted-unifrac-stagnation-permdisp.qzv \
 --p-pairwise
qiime diversity beta-group-significance \
 --i-distance-matrix core-metrics-results/unweighted unifrac distance matrix.qza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --m-metadata-column Material \
 --p-method 'permdisp' \
 --o-visualization core-metrics-results/unweighted-unifrac-material-permdisp.qzv \
 --p-pairwise
qiime emperor plot \
 --i-pcoa core-metrics-results/unweighted unifrac pcoa results.gza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --o-visualization core-metrics-results/unweighted-unifrac-emperor.qzv
qiime emperor plot \
 --i-pcoa core-metrics-results/bray curtis pcoa results.qza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --o-visualization core-metrics-results/bray-curtis-emperor.qzv
giime feature-classifier classify-sklearn \
 --i-classifier gg-13-8-99-515-806-nb-classifier.qza \
 --i-reads rep-seqs.qza \
 --o-classification taxonomy.gza
giime metadata tabulate \
 --m-input-file taxonomy.gza \
 --o-visualization taxonomy.qzv
qiime taxa barplot \
 --i-table table.qza \
 --i-taxonomy taxonomy.qza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --o-visualization taxa-bar-plots.qzv
qiime feature-table filter-samples \
```

- --i-table table.qza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --p-where "[Wall]='W1'" \
- --o-filtered-table W1-table.qza

giime composition add-pseudocount \

- --i-table W1-table.gza \
- --o-composition-table comp-W1-table.qza

qiime composition ancom \

- --i-table comp-W1-table.qza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --m-metadata-column Material \
- --o-visualization ancom-W1-Material.qzv

qiime taxa collapse \

- --i-table W1-table.qza \
- --i-taxonomy taxonomy.qza \
- --p-level 6 \
- --o-collapsed-table W1-table-I6.qza

qiime composition add-pseudocount \

- --i-table W1-table-I6.qza \
- --o-composition-table comp-W1-table-l6.qza

qiime composition ancom \

- --i-table comp-W1-table-I6.qza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --m-metadata-column Material \
- --o-visualization I6-ancom-W1-Material.qzv

qiime feature-table summarize \

- --i-table rarefied_table.qza \
- --o-visualization rarefied table.qzv \
- --m-sample-metadata-file AliyaMetaDataNew.tsv

THIS WORKS for filtering results

giime feature-table filter-samples \

- --i-table table.qza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --p-where "[MonthlyFlush]='yes'" \
- --o-filtered-table MonthFlush-filtered-table.qza

giime feature-table summarize \

- --i-table MonthFlush-filtered-table.qza \
- --o-visualization MonthFlush-filtered-table.qzv \
- --m-sample-metadata-file AliyaMetaDataNew.tsv

qiime feature-table filter-samples \

- --i-table table.qza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --p-where "[Experiment]='Stagnation'" \
- --o-filtered-table Stag-NoMonth0-filtered-table.qza

qiime feature-table summarize \

- --i-table Stag-NoMonth0-filtered-table.qza \
- --o-visualization Stag-NoMonth0-filtered-table.qzv \
- --m-sample-metadata-file AliyaMetaDataNew.tsv

qiime feature-table filter-samples \

- --i-table MonthFlush-filtered-table.gza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --p-where "[SampleType]='Sample'" \
- --o-filtered-table MonthFlush-filtered-table-NoBlank.gza

giime feature-table summarize \

- --i-table MonthFlush-filtered-table-NoBlank.qza \
- --o-visualization MonthFlush-filtered-table-NoBlank.qzv \
- --m-sample-metadata-file AliyaMetaDataNew.tsv

giime feature-table filter-samples \

- --i-table Stag-NoMonth0-filtered-table.qza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --p-where "[SampleType]='Sample'" \
- --o-filtered-table Stag-NoMonth0-filtered-table-NoBlank.gza

qiime feature-table summarize \

- --i-table Stag-NoMonth0-filtered-table-NoBlank.gza \
- --o-visualization Stag-NoMonth0-filtered-table-NoBlank.qzv \
- --m-sample-metadata-file AliyaMetaDataNew.tsv

qiime diversity core-metrics-phylogenetic \

- --i-phylogeny rooted-tree.qza \
- --i-table MonthFlush-filtered-table.qza \
- --p-sampling-depth 20980 \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --output-dir core-metrics-results-MonthFlush

qiime diversity core-metrics-phylogenetic \

- --i-phylogeny rooted-tree.qza \
- --i-table Stag-NoMonth0-filtered-table-NoBlank.gza \
- --p-sampling-depth 20980 \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --output-dir core-metrics-results-MonthFlush-NoMonth0

#Random Forest

qiime sample-classifier classify-samples \

- --i-table MonthFlush-filtered-table.qza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --m-metadata-column StagType \
- --p-optimize-feature-selection \
- --p-parameter-tuning \
- --p-estimator RandomForestClassifier \
- --p-n-estimators 20 \
- --p-test-size 0.2 \
- --output-dir MonthFlush-classifier

qiime metadata tabulate \

- --m-input-file MonthFlush-classifier/predictions.qza \
- --o-visualization MonthFlush-classifier/predictions.gzv

qiime metadata tabulate \

- --m-input-file MonthFlush-classifier/probabilities.gza \
- --o-visualization MonthFlush-classifier/probabilities.gzv

qiime metadata tabulate \

- --m-input-file MonthFlush-classifier/feature_importance.qza \
- --o-visualization MonthFlush-classifier/feature_importance.qzv

qiime feature-table filter-features \

- --i-table MonthFlush-filtered-table.qza \
- --m-metadata-file MonthFlush-classifier/feature_importance.qza \

--o-filtered-table MonthFlush-classifier/important-feature-table.qza

qiime sample-classifier heatmap \

- --i-table MonthFlush-filtered-table.qza \
- --i-importance MonthFlush-classifier/feature importance.gza \
- --m-sample-metadata-file AliyaMetaDataNew.tsv \
- --m-sample-metadata-column StagType \
- --p-group-samples \
- --p-feature-count 30 \
- --o-filtered-table MonthFlush-classifier/important-feature-table-top-30.gza \
- --o-heatmap MonthFlush-classifier/important-feature-heatmap.qzv

qiime sample-classifier heatmap \

- --i-table MonthFlush-filtered-table.qza \
- --i-importance MonthFlush-classifier/feature importance.gza \
- --m-sample-metadata-file AliyaMetaDataNew.tsv \
- --m-sample-metadata-column StagType \
- --m-feature-metadata-file taxonomy.qza \
- --m-feature-metadata-column Taxon \
- --p-group-samples \
- --p-feature-count 30 \
- --o-filtered-table MonthFlush-classifier/important-feature-table-taxonomy-top-30.qza \
- --o-heatmap MonthFlush-classifier/important-feature-heatmap-taxonomy.qzv

#Stats for Monthly Flush

giime diversity alpha-correlation \

- --i-alpha-diversity core-metrics-results-MonthFlush/faith_pd_vector.qza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --o-visualization core-metrics-results-MonthFlush/faith-pd-alpha-correlation.gzv

giime diversity alpha-correlation \

- --i-alpha-diversity core-metrics-results-MonthFlush/shannon vector.gza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --o-visualization core-metrics-results-MonthFlush/shannon-group-correlation.gzv

qiime diversity alpha-group-significance \

- --i-alpha-diversity core-metrics-results-MonthFlush/observed features vector.qza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --o-visualization core-metrics-results-MonthFlush/observed_features-group-significance.qzv

qiime diversity alpha-group-significance \

```
--i-alpha-diversity core-metrics-results-MonthFlush/evenness vector.gza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --o-visualization core-metrics-results-MonthFlush/evenness-group-significance.qzv
qiime diversity beta-group-significance \
 --i-distance-matrix core-metrics-results-MonthFlush/bray curtis distance matrix.qza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --m-metadata-column StagType \
 --o-visualization core-metrics-results-MonthFlush/bray_curtis-StagType-group-significance.qzv
 --p-pairwise
qiime diversity beta-group-significance \
 --i-distance-matrix core-metrics-results-MonthFlush/jaccard_distance_matrix.qza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --m-metadata-column StagType \
 --o-visualization core-metrics-results-MonthFlush/jaccard-StagType-group-significance.gzv \
 --p-pairwise
qiime diversity beta-group-significance \
 --i-distance-matrix core-metrics-results-MonthFlush/weighted unifrac distance matrix.gza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --m-metadata-column StagType \
 --o-visualization
core-metrics-results-MonthFlush/weighted-unifrac-StagType-group-significance.qzv \
 --p-pairwise
qiime diversity beta-group-significance \
 --i-distance-matrix core-metrics-results-MonthFlush/unweighted_unifrac_distance_matrix.qza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --m-metadata-column StagType \
 --o-visualization
core-metrics-results-MonthFlush/unweighted-unifrac-StagType-group-significance.qzv \
 --p-pairwise
######### ANCOM
giime feature-table filter-samples \
 --i-table MonthFlush-filtered-table.gza \
 --m-metadata-file AliyaMetaDataNew.tsv \
 --p-where "[Wall]='W1'" \
 --o-filtered-table Month-Flush-W1-table.qza
qiime composition add-pseudocount \
 --i-table Month-Flush-W1-table.qza \
```

--o-composition-table comp-Month-Flush-W1-table.gza qiime composition ancom \ --i-table comp-Month-Flush-W1-table.gza \ --m-metadata-file AliyaMetaDataNew.tsv \ --m-metadata-column Material \ --o-visualization ancom-Month-Flush-W1-Material.gzv qiime taxa collapse \ --i-table Month-Flush-W1-table.qza \ --i-taxonomy taxonomy.qza \ --p-level 6 \ --o-collapsed-table Month-Flush-W1-table-I6.qza qiime composition add-pseudocount \ --i-table Month-Flush-W1-table-I6.qza \ --o-composition-table comp-Month-Flush-W1-table-l6.qza qiime composition ancom \ --i-table comp-Month-Flush-W1-table-I6.gza \ --m-metadata-file AliyaMetaDataNew.tsv \ --m-metadata-column Material \ --o-visualization I6-ancom-Month-Flush-W1-Material.gzv #PieCrust2 qiime picrust2 full-pipeline \ --i-table MonthFlush-filtered-table.gza \ --i-seq rep-seqs.qza \ --output-dir q2-picrust2_output \ --p-placement-tool sepp \ --p-threads 4 \ --p-hsp-method pic \ --p-max-nsti 2 \ --verbose # Trying to fix weird piecrust error qiime dada2 denoise-paired \ --i-demultiplexed-seqs demux-full-new.qza \ --p-trim-left-f 0 \

--p-trim-left-r 0 \

- --p-trunc-len-f 195 \
- --p-trunc-len-r 205 \
- --o-table table-oldQiime.qza \
- --o-representative-sequences rep-seqs-oldQiime.qza \
- --o-denoising-stats denoising-stats-oldQiime.qza

qiime feature-table filter-samples \

- --i-table table-oldQiime.qza \
- --m-metadata-file AliyaMetaDataNew.tsv \
- --p-where "[MonthlyFlush]='yes'" \
- --o-filtered-table MonthFlush-filtered-table-oldQiime.qza